OYCO 02-26-01

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RAW SEQUENCE LISTING   DATE: 02/14/2001
PATENT APPLICATION: US/09/775,803   TIME: 16:33:28

ENTERED

Input Set : A:\Co5044us.txt
Output Set: N:\CRF3\02142001\I775803.raw

#2.

```
       3 <110> APPLICANT: COR Therapeutics, Inc.
       4        Ramakrishnan, Vanitha
       5        Phillips, David
       7 <120> TITLE OF INVENTION: Transgenic Animals Having a Modified Glycoprotein V
       8        Gene and Methods for Their Use
      10 <130> FILE REFERENCE: 44481-5044-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/775,803
C--> 13 <141> CURRENT FILING DATE: 2001-02-05
      15 <150> PRIOR APPLICATION NUMBER: PCT/US99/17594
      16 <151> PRIOR FILING DATE: 1999-08-04
      18 <150> PRIOR APPLICATION NUMBER: US 60/109,797
      19 <151> PRIOR FILING DATE: 1998-08-04
      21 <160> NUMBER OF SEQ ID NOS: 14
      23 <170> SOFTWARE: PatentIn Ver. 2.1
      25 <210> SEQ ID NO: 1
      26 <211> LENGTH: 20
      27 <212> TYPE: DNA
      28 <213> ORGANISM: Artificial Sequence
      30 <220> FEATURE:
      31 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
      33 <220> FEATURE:
      34 <221> NAME/KEY: variation
      35 <222> LOCATION: (13)..(18)
      36 <223> OTHER INFORMATION: y at position 13 = c or t; r at position 18 = a or
      37        g.
      39 <400> SEQUENCE: 1
      40    ggcatgaccg tcytgcarcg                                      20
      43 <210> SEQ ID NO: 2
      44 <211> LENGTH: 7
      45 <212> TYPE: PRT
      46 <213> ORGANISM: Homo sapiens
      48 <220> FEATURE:
      49 <223> OTHER INFORMATION: Amino acid sequence corresponding to primer of
      50        seq. id no. 5.
      52 <400> SEQUENCE: 2
      53    Gly Met Thr Val Leu Gln Arg
      54      1               5
      57 <210> SEQ ID NO: 3
      58 <211> LENGTH: 23
      59 <212> TYPE: DNA
      60 <213> ORGANISM: Artificial Sequence
      62 <220> FEATURE:
      63 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
      65 <220> FEATURE:
      66 <221> NAME/KEY: variation
      67 <222> LOCATION: (3)..(21)
      68 <223> OTHER INFORMATION: y at position 3 = c or t; r at positions 6 and 21
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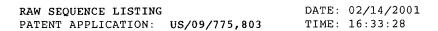Output Set: N:\CRF3\02142001\I775803.raw

```
69          = a or g.
71 <400> SEQUENCE: 3
72     gayaaratgg tgytcytgga rca                                     23
75 <210> SEQ ID NO: 4
76 <211> LENGTH: 8
77 <212> TYPE: PRT
78 <213> ORGANISM: Homo sapiens
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Amino acid sequence corresponding to primer of
82        seq. id no. 7.
84 <400> SEQUENCE: 4
85    Asp Lys Met Val Leu Leu Glu Gln
86        1             5
89 <210> SEQ ID NO: 5
90 <211> LENGTH: 26
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
97 <220> FEATURE:
98 <221> NAME/KEY: variation
99 <222> LOCATION: (3)..(24)
100 <223> OTHER INFORMATION: y at positions 3, 12, 15, 18 and 19 = c or t; v at
101        position 6 = a or c or g; m at position 9 = a or
102        c; s at position 24 = c or g.
104 <400> SEQUENCE: 5
105     ccyggvacmt tyagygayyt gatsaa                                 26
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 9
110 <212> TYPE: PRT
111 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 6
114     Pro Gly Thr Phe Ser Asp Leu Ile Lys
115        1             5
118 <210> SEQ ID NO: 7
119 <211> LENGTH: 21
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
126 <220> FEATURE:
127 <221> NAME/KEY: variation
128 <222> LOCATION: (1)..(19)
129 <223> OTHER INFORMATION: r at positions 1, 7, 10, 13, 16 and 19 = a or g;
130        b at position 4 = c or g or t; k at position 6 =
131        g or t.
133 <400> SEQUENCE: 7
134     rttbckraar gcrgcrgcrg g                                      21
137 <210> SEQ ID NO: 8
```

```
138 <211> LENGTH: 7
139 <212> TYPE: PRT
140 <213> ORGANISM: Homo sapiens
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Amino acid sequence corresponding to the
144       complementary strand of the primer in seq. id no.
145       11.
147 <400> SEQUENCE: 8
148    Pro Ala Ala Ala Phe Arg Asn
149    1               5
152 <210> SEQ ID NO: 9
153 <211> LENGTH: 29
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
160 <220> FEATURE:
161 <221> NAME/KEY: variation
162 <222> LOCATION: (8)..(27)
163 <223> OTHER INFORMATION: r at positions 8, 12, 15, 18, 23 and 27 = a or g;
164       k at position 9 = g or t.
166 <400> SEQUENCE: 9
167    ggccccarkc crcartcrca garccarga                          29
170 <210> SEQ ID NO: 10
171 <211> LENGTH: 9
172 <212> TYPE: PRT
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 10
176    Ser Trp Arg Cys Asp Cys Gly Leu Gly
177    1               5
180 <210> SEQ ID NO: 11
181 <211> LENGTH: 3586
182 <212> TYPE: DNA
183 <213> ORGANISM: Mus musculus
185 <220> FEATURE:
186 <221> NAME/KEY: CDS
187 <222> LOCATION: (1411)..(3108)
188 <223> OTHER INFORMATION: Platelet glycoprotein V gene
190 <400> SEQUENCE: 11
191    gaattcattg gccttattta agaaataaaa tgttgagcaa aagagatggc tcatcaggta 60
193    aagatacctc ccaagacatg gtgtgagtcc ttgggaacct acgtggagga aggtgagaac 120
195    caattgccta aagttttctg acacccacaa gtgaggcact gccacatgca cccacatact 180
197    cctgcacagg aatgagttag tgcaatgtag catggaaaaa aaccaaaagt gtggcccatg 240
199    taatgacagc ctgctatttc tgggaaaact taggccctct actctctagc ttttacaaaa 300
201    ggacttttaa ctatggactc tgaaagtttg aaagctcttg tcattaaaac ctagaatatg 360
203    ccctatggag atagtctttt tcttgacttt ttatctggta aggtctttat cttgaggatg 420
205    caagaatact tccctcttcc tctctgaagt gccaagtcac aagcagagct gcaagccttt 480
207    cagtcagtcc agggtgcaga actgcttcag gtaaggccaa atattcttaa attagtgtat 540
209    gcagttagag gctcagtctg tataggggca gaaggagacc tggtacaaga aacagtacaa 600
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211   atttttactt gggaaacaga gtaaactagt attactgtgt gcttcctggg taactcaatg 660
213   cccagagtag ttttattaag cagcttggtg tataagcaaa cagtagctca ttatttaaat 720
215   gtgtgagtca gaaaaacatc ttcaaatgct acttatgtga cacttaaatt aacctcatgt 780
217   acactggagc gaccagccta ctgcactcgt gttactgtaa cagtgcaaag ttcagaaaag 840
219   catggcataa agcaatgggc attatcacct gcaccactgg gctccgggcc gggagttaca 900
221   aaacggtgta atgagttgtg gggtgttggt actttgaaaa tatgtaagaa attgaatcta 960
223   gtggaagtgg gccttgctgc ggttctcttg ctgactgttg gggataaagc tccctgctta 1020
225   acttgttaaa gtcagtgaca cagccagtcc caggaggcgt tgctttctat tctctgaaaa 1080
227   agaccgtagc aattttaatt cgttctgtaa cgattttaag gtattctgta gcttgaaaat 1140
229   gcccaaatgt caatgctcta aacagaaccg gggagatggc tgactggata aaaatgggaa 1200
231   cctgtaagac tgatctactc tccaataccc acatatgctg aatagaaaag taattttttt 1260
233   ttaatcagcc tttgtaagat agaggaagac ttggttgtat ctgagcgttc caaggccgtg 1320
235   agagtgctgg cccaaaaact gtgcttgcag cagtgcgtgc agggctccag gatatgctct 1380
237   gagccttgtt tttgctcttg catttcagac atg cta aga agc gcc ctg ctg tcc 1434
238                                      Met Leu Arg Ser Ala Leu Leu Ser
239                                       1               5
241   gcg gtg ctc gca ctc ttg cgt gcc caa cct ttt ccc tgc ccc aaa acc 1482
242   Ala Val Leu Ala Leu Leu Arg Ala Gln Pro Phe Pro Cys Pro Lys Thr
243        10              15                  20
245   tgc aag tgt gtg gtc cgc gat gcc gcg cag tgc tcg ggc ggc agc gtg 1530
246   Cys Lys Cys Val Val Arg Asp Ala Ala Gln Cys Ser Gly Gly Ser Val
247    25              30                  35                  40
249   gct cac atc gct gag cta ggt ctg cct acg aac ctc aca cac atc ctg 1578
250   Ala His Ile Ala Glu Leu Gly Leu Pro Thr Asn Leu Thr His Ile Leu
251                45                  50                  55
253   ctc ttc cga atg gac cag ggc ata ttg cgg aac cac agc ttc agc ggc 1626
254   Leu Phe Arg Met Asp Gln Gly Ile Leu Arg Asn His Ser Phe Ser Gly
255                60                  65                  70
257   atg aca gtc ctt cag cgc ctg atg ctc tca gat agc cac att tcc gcc 1674
258   Met Thr Val Leu Gln Arg Leu Met Leu Ser Asp Ser His Ile Ser Ala
259                75                  80                  85
261   atc gac ccc ggc acc ttc aat gac ctg gta aaa ctg aaa acc ctc agg 1722
262   Ile Asp Pro Gly Thr Phe Asn Asp Leu Val Lys Leu Lys Thr Leu Arg
263        90                  95                  100
265   ttg acg cgc aac aaa atc tct cgt ctt cca cgt gcg atc ctg gat aag 1770
266   Leu Thr Arg Asn Lys Ile Ser Arg Leu Pro Arg Ala Ile Leu Asp Lys
267   105                 110                 115                 120
269   atg gta ctc ttg gaa cag ctg ttc ttg gac cac aat gca cta agg gac 1818
270   Met Val Leu Leu Glu Gln Leu Phe Leu Asp His Asn Ala Leu Arg Asp
271                125                 130                 135
273   ctt gat caa aac ctg ttt cag caa ctg cgt aac ctt cag gag ctc ggt 1866
274   Leu Asp Gln Asn Leu Phe Gln Gln Leu Arg Asn Leu Gln Glu Leu Gly
275                140                 145                 150
277   ttg aac cag aat cag ctc tct ttt ctt cct gct aac ctt ttc tcg agc 1914
278   Leu Asn Gln Asn Gln Leu Ser Phe Leu Pro Ala Asn Leu Phe Ser Ser
279        155                 160                 165
281   ctg aga gaa ctg aag ttg ttg gat tta tcg cga aac aac ctg acc cac 1962
282   Leu Arg Glu Leu Lys Leu Leu Asp Leu Ser Arg Asn Asn Leu Thr His
283        170                 175                 180
```

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```
285    ctg ccc aag gga ctg ctt ggg gct caa gtt aag ctt gag aaa ctg ctg    2010
286    Leu Pro Lys Gly Leu Leu Gly Ala Gln Val Lys Leu Glu Lys Leu Leu
287    185             190                 195                 200
289    ctc tat tca aac cag ctc acg tct gtg gat tcg ggg ctg ctg agc aac    2058
290    Leu Tyr Ser Asn Gln Leu Thr Ser Val Asp Ser Gly Leu Leu Ser Asn
291                    205                 210                 215
293    ctg ggc gcc ctg act gag ctg cgg ctg gag cgg aat cac ctc cgc tcc    2106
294    Leu Gly Ala Leu Thr Glu Leu Arg Leu Glu Arg Asn His Leu Arg Ser
295                    220                 225                 230
297    gta gcc ccg ggt gcc ttc gac cgc ctc gga aac ctg agc tcc ttg act    2154
298    Val Ala Pro Gly Ala Phe Asp Arg Leu Gly Asn Leu Ser Ser Leu Thr
299            235                 240                 245
301    cta tcc gga aac ctc ctg gag tct ctg ccg ccc gcg ctc ttc ctt cac    2202
302    Leu Ser Gly Asn Leu Leu Glu Ser Leu Pro Pro Ala Leu Phe Leu His
303            250                 255                 260
305    gtg agc agc gtg tct cgg ctg act ctg ttc gag aac ccc ctg gag gag    2250
306    Val Ser Ser Val Ser Arg Leu Thr Leu Phe Glu Asn Pro Leu Glu Glu
307    265                 270                 275                 280
309    ctc ccg gac gtg ttg ttc ggg gag atg gcc ggc ctg cgg gag ctg tgg    2298
310    Leu Pro Asp Val Leu Phe Gly Glu Met Ala Gly Leu Arg Glu Leu Trp
311                    285                 290                 295
313    ctg aac ggc acc cac ctg agc acg ctg ccc gcc gct gcc ttc cgc aac    2346
314    Leu Asn Gly Thr His Leu Ser Thr Leu Pro Ala Ala Ala Phe Arg Asn
315                    300                 305                 310
317    ctg agc ggc ttg cag acg ctg ggg ctg acg cgg aac ccg cgc ctg agc    2394
318    Leu Ser Gly Leu Gln Thr Leu Gly Leu Thr Arg Asn Pro Arg Leu Ser
319            315                 320                 325
321    gcg ctc ccg cgc ggc gtg ttc cag ggc cta cgg gag ctg cgc gtg ctc    2442
322    Ala Leu Pro Arg Gly Val Phe Gln Gly Leu Arg Glu Leu Arg Val Leu
323            330                 335                 340
325    gcg ctg cac acc aac gcc ctg gcg gag ctg cgg gac gac gcg ctg cgc    2490
326    Ala Leu His Thr Asn Ala Leu Ala Glu Leu Arg Asp Asp Ala Leu Arg
327    345                 350                 355                 360
329    ggc ctc ggg cac ctg cgc cag gtg tcg ctg cgc cac aac cgg ctg cgg    2538
330    Gly Leu Gly His Leu Arg Gln Val Ser Leu Arg His Asn Arg Leu Arg
331                    365                 370                 375
333    gcc ctg ccc cgc acg ctc ttc cgc aac ctc agc agc ctc gag agc gtg    2586
334    Ala Leu Pro Arg Thr Leu Phe Arg Asn Leu Ser Ser Leu Glu Ser Val
335            380                 385                 390
337    cag cta gag cac aac cag ctg gag acg ctg cca gga gac gtg ttc gcg    2634
338    Gln Leu Glu His Asn Gln Leu Glu Thr Leu Pro Gly Asp Val Phe Ala
339            395                 400                 405
341    gct ctg ccc cag ctg acc cag gtc ctg ctg ggt cac aac ccc tgg ctc    2682
342    Ala Leu Pro Gln Leu Thr Gln Val Leu Leu Gly His Asn Pro Trp Leu
343            410                 415                 420
345    tgc gac tgt ggc ctg tgg ccc ttc ctc cag tgg ctg cgg cat cac ccg    2730
346    Cys Asp Cys Gly Leu Trp Pro Phe Leu Gln Trp Leu Arg His His Pro
347    425                 430                 435                 440
349    gac atc ctg ggc cga gac gag ccc ccg cag tgc cgt ggc ccg gag cca    2778
```

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date